CLAIMS

1. An isolated peptide scaffold for β-turn display comprising a presented turn sequence flanked by two opposite strands with a defined backbone hydrogen-bonding pattern, each strand comprising at least two Trp residues at non-hydrogen-bonded positions, wherein the Trp residues form a cross-strand zipper-like motif without any disulfide bond.

2. The peptide scaffold of claim 1, wherein the presented turn sequence comprises at least 4 amino acids.

3. The peptide scaffold of claim 1, wherein the presented turn sequence comprises at least 6 amino acids

4. The peptide scaffold of claim 1, wherein the flanking strand consists of naturally occurring L-form amino acids.

5. The peptide scaffold of claim 1, wherein each flanking strand is at least 3 amino acids in length.

6. The peptide scaffold of claim 1 comprising at least 10 amino acids.

7. The peptide scaffold of claim 6 comprising no more than 20 amino acids.

8. The peptide scaffold of claim 7 comprising about 12 amino acids.

9. The peptide scaffold of claim 7 comprising about 16 amino acids.

10. A library of structurally-constrained peptides, each peptide comprises a presented turn sequence consisting of random amino acids, said turn sequence flanked by two opposite strands with a defined backbone hydrogen-bonding pattern, said each strand comprising at least two Trp residues at non-hydrogen-bonded positions, wherein the Trp residues of the scaffold form a cross-strand zipper-like motif without any disulfide bond.

11. The library of claim 10, wherein the presented turn sequence comprises at least 4 amino acids.

12. The library of claim 10, wherein the presented turn sequence comprises at least 6 amino acids.

13. The library of claim 10, wherein each flanking strand consists of naturally occurring L-form amino acids.

14. The library of claim 10, wherein each flanking strand is at least 3 amino acids in length.

15. The library of claim 10, wherein each peptide comprises at least 10 amino acids.

16. The library of claim 10, wherein each peptide comprises no more than 20 amino acids.

17. The library of claim 16, wherein each peptide comprises about 12 amino acids.

18. The library of claim 16, wherein each peptide comprises about 16 amino acids.

19. A method of constructing a library of structurally-constrained peptides comprising synthesizing a plurality of peptides having the scaffold of claim 1, wherein the presented turn sequence consists of random amino acids.

20. The method of claim 19, wherein the presented turn sequence comprises at least 4 amino acids.

21. The method of claim 19, wherein the presented turn sequence comprises at least 6 amino acids

22. The method of claim 19, wherein each flanking strand consists of naturally occurring L-form amino acids.

23. The method of claim 19, wherein each flanking strand is at least 3 amino acids in length.

24. The method of claim 19, wherein each peptide comprises at least 10 amino acids.

25. The method of claim 19, wherein each peptide comprises no more than 20 amino acids.

26. The method of claim 25, wherein each peptide comprises about 12 amino acids.

27. The method of claim 25, wherein each peptide comprises about 16 amino acids.

28. A method of identifying peptides that bind to a bioactive target molecule, comprising the steps of:

a) providing a library of claim 10;

b) contacting the library with the target molecule;

c) selecting from the library peptides that form a noncovalent complex with the target molecule; and

d) optionally isolating the peptides selected in step c).